

BATCH

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/587,111

DATE: 02/14/2001
TIME: 10:17:25

Input Set : A:\587111.txt
Output Set: N:\CRF3\02142001\I587111.raw

3 <110> APPLICANT: Curtis, Rory A.J.
5 <120> TITLE OF INVENTION: NOVEL MEMBERS OF THE CAPSAICIN/VANILLOID RECEPTOR
6 FAMILY OF PROTEINS AND USES THEREOF
8 <130> FILE REFERENCE: MNI-062CP2
10 <140> CURRENT APPLICATION NUMBER: US/09/587,111
11 <141> CURRENT FILING DATE: 2000-06-02
13 <150> PRIOR APPLICATION NUMBER: US/09/439,165
14 <151> PRIOR FILING DATE: 1999-11-12
16 <150> PRIOR APPLICATION NUMBER: 60/108,322
17 <151> PRIOR FILING DATE: 1998-11-13
19 <150> PRIOR APPLICATION NUMBER: 60/114,078
20 <151> PRIOR FILING DATE: 1998-12-28
22 <150> PRIOR APPLICATION NUMBER: 09/258,633
23 <151> PRIOR FILING DATE: 1999-02-26
25 <150> PRIOR APPLICATION NUMBER: 09/421,134
26 <151> PRIOR FILING DATE: 1999-10-19
28 <160> NUMBER OF SEQ ID NOS: 20
30 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 3909
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1113)..(3629)
41 <400> SEQUENCE: 1
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46 cgcaacgcac tgcgggcagt gagcgcaacg cactgcgggc agtgagcgca acgcacttgc 180
48 gggcagtgcg cgcaacgcac tgcgggcagt gagcgcaacg cactgcgggc agtgagcgca 240
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52 gtgagcgcaa cgactgcgg gcagtgcgcg caacgcactg cgggcagtga ggcgaacgca 360
54 ctgcgggagcag tgagcgcaac gcaactgcggg cagtgcgcgc aacgcactgc gggcagtgcg 420
56 cgcaacgcac ttaattgtgcg ttagctcact cattaaggcag cccaggcttt acactttatg 480
58 cttccggctc gtatgtgtgcg tgggaattgtg agcggataac aatttcacac aggaaacagc 540
60 tatgaccatg attacgcaa gctctaatac gactcactat agggaaagct ggtacgcctg 600
62 caggtaaccg tccggaattc ccgggtcgac ccacgcgtcc gaaaacacac ctctctgctg 660
64 tgggaagact gtgcaatggc acagccgcag agcttggttt gggaggttga agtgctctgcg 720
66 ggagaattcg tagatcatcc tcagaaaagc cttgcccctg tgttctacca gaaaaacgct 780
68 tcccaatcac ccagaaaagc tgtccacagt agtccccctt tatccacggg tgtaactttc 840
70 catgggttca gttatttgcg gtcaaccacg gtctgccaat attaaatgga aaattcttca 900
72 aacagttccc aagttttccc ttgtgcattg ttctgagcag tgtgatgaag agtctctgcc 960
74 gtgcatctgc ggtatgcaac cgtccctgtg tccccacgt ccaggccgta gatgctcccc 1020
76 gccggtcagt cacttagtcg tcagatgcgc cgtccctgta tcacagtgcg tctgttcagg 1080
78 ttgcacactg ggccacagag gatccagcaa gg atg aag aaa tgg agc agc aca 1133
79 Met Lys Lys Trp Ser Ser Thr
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82 gac ttg ggg aca gct gcg gac cca ctc caa aag gac acc tgc cca gac 1181
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86 ccc ctg gat gga gac cct aac tcc agg cca cct cca gcc aag ccc cag 1229
87 Pro Leu Asp Gly Asp Pro Asn Ser Arg Pro Pro Pro Ala Lys Pro Gln
88      25      30      35
90 ctc ccc acg gcc aag agc cgc acc cgg ctc ttt ggg aag ggt gac tcg 1277
91 Leu Pro Thr Ala Lys Ser Arg Thr Arg Leu Phe Gly Lys Gly Asp Ser
92      40      45      50      55
94 gag gag gct ttc ccg gtg gat tgc ccc cac gag gaa ggt gag ttg gac 1325
95 Glu Glu Ala Phe Pro Val Asp Cys Pro His Glu Glu Gly Glu Leu Asp
96      60      65      70
98 tcc tgc ccg acc atc aca gtc agc cct gtt atc acc atc cag agg cca 1373
99 Ser Cys Pro Thr Ile Thr Val Ser Pro Val Ile Thr Ile Gln Arg Pro
100      75      80      85
102 gga gac ggc ccc acc ggt gcc agg ctg ctg tcc cag gac tct gtc gcc 1421
103 Gly Asp Gly Pro Thr Gly Ala Arg Leu Leu Ser Gln Asp Ser Val Ala
104      90      95      100
106 gcc agc acc gag aag acc ctc agg ctc tat gat cgc agg agt atc ttt 1469
107 Ala Ser Thr Glu Lys Thr Leu Arg Leu Tyr Asp Arg Arg Ser Ile Phe
108      105      110      115
110 gaa gcc gtt gct cag aat aac tgc cag gat ctg gag agc ctg ctg ctc 1517
111 Glu Ala Val Ala Gln Asn Asn Cys Gln Asp Leu Glu Ser Leu Leu Leu
112      120      125      130      135
114 ttc ctg cag aag agc aag aag cac ctc aca gac aac gag ttc aaa gac 1565
115 Phe Leu Gln Lys Ser Lys Lys His Leu Thr Asp Asn Glu Phe Lys Asp
116      140      145      150
118 cct gag aca ggg aag acc tgt ctg ctg aaa gcc atg ctc aac ctg cac 1613
119 Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys Ala Met Leu Asn Leu His
120      155      160      165
122 gac gga cag aac acc acc atc ccc ctg ctc ctg gag atc gcg cgg caa 1661
123 Asp Gly Gln Asn Thr Thr Ile Pro Leu Leu Leu Glu Ile Ala Arg Gln
124      170      175      180
126 acg gac agc ctg aag gag ctt gtc aac gcc agc tac acg gac agc tac 1709
127 Thr Asp Ser Leu Lys Glu Leu Val Asn Ala Ser Tyr Thr Asp Ser Tyr
128      185      190      195
130 tac aag ggc cag aca gca ctg cac atc gcc atc gag aga cgc aac atg 1757
131 Tyr Lys Gly Gln Thr Ala Leu His Ile Ala Ile Glu Arg Arg Asn Met
132      200      205      210      215
134 gcc ctg gtg acc ctc ctg gtg gag aac gga gca gac gtc cag gct gcg 1805
135 Ala Leu Val Thr Leu Val Glu Asn Gly Ala Asp Val Gln Ala Ala
136      220      225      230
138 gcc cat ggg gac ttc ttt aag aaa acc aaa ggg cgg cct gga ttc tac 1853
139 Ala His Gly Asp Phe Phe Lys Lys Thr Lys Gly Arg Pro Gly Phe Tyr
140      235      240      245
142 ttc ggt gaa ctg ccc ctg tcc ctg gcc gcg tgc acc aac cag ctg ggc 1901
143 Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Asn Gln Leu Gly
144      250      255      260
146 atc gtg aag ttc ctg ctg cag aac tcc tgg cag acg gcc gac atc agc 1949

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147	Ile	Val	Lys	Phe	Leu	Leu	Gln	Asn	Ser	Trp	Gln	Thr	Ala	Asp	Ile	Ser	
148		265					270					275					
150	gcc	agg	gac	tcg	gtg	ggc	aac	acg	gtg	ctg	cac	gcc	ctg	gtg	gag	gtg	1997
151	Ala	Arg	Asp	Ser	Val	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Glu	Val	
152	280					285					290				295		
154	gcc	gac	aac	acg	gcc	gac	aac	acg	aag	ttt	gtg	acg	agc	atg	tac	aat	2045
155	Ala	Asp	Asn	Thr	Ala	Asp	Asn	Thr	Lys	Phe	Val	Thr	Ser	Met	Tyr	Asn	
156					300					305					310		
158	gag	att	ctg	atg	ctg	ggg	gcc	aaa	ctg	cac	ccg	acg	ctg	aag	ctg	gag	2093
159	Glu	Ile	Leu	Met	Leu	Gly	Ala	Lys	Leu	His	Pro	Thr	Leu	Lys	Leu	Glu	
160				315					320					325			
162	gag	ctc	acc	aac	aag	aag	gga	atg	acg	ccg	ctg	gct	ctg	gca	gct	ggg	2141
163	Glu	Leu	Thr	Asn	Lys	Lys	Gly	Met	Thr	Pro	Leu	Ala	Leu	Ala	Ala	Gly	
164			330					335					340				
166	acc	ggg	aag	atc	ggg	gtc	ttg	gcc	tat	att	ctc	cag	cgg	gag	atc	cag	2189
167	Thr	Gly	Lys	Ile	Gly	Val	Leu	Ala	Tyr	Ile	Leu	Gln	Arg	Glu	Ile	Gln	
168		345				350					355						
170	gag	ccc	gag	tgc	agg	cac	ctg	tcc	agg	aag	ttc	acc	gag	tgg	gcc	tac	2237
171	Glu	Pro	Glu	Cys	Arg	His	Leu	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Ala	Tyr	
172	360					365				370					375		
174	ggg	ccc	gtg	cac	tcc	tcg	ctg	tac	gac	ctg	tcc	tgc	atc	gac	acc	tgc	2285
175	Gly	Pro	Val	His	Ser	Ser	Leu	Tyr	Asp	Leu	Ser	Cys	Ile	Asp	Thr	Cys	
176				380					385					390			
178	gag	aag	aac	tcg	gtg	ctg	gag	gtg	atc	gcc	tac	agc	agc	agc	gag	acc	2333
179	Glu	Lys	Asn	Ser	Val	Leu	Glu	Val	Ile	Ala	Tyr	Ser	Ser	Ser	Glu	Thr	
180			395					400					405				
182	cct	aat	cgc	cac	gac	atg	ctc	ttg	gtg	gag	ccg	ctg	aac	cga	ctc	ctg	2381
183	Pro	Asn	Arg	His	Asp	Met	Leu	Leu	Val	Glu	Pro	Leu	Asn	Arg	Leu	Leu	
184		410					415					420					
186	cag	gac	aag	tgg	gac	aga	ttc	gtc	aag	cgc	atc	ttc	tac	ttc	aac	ttc	2429
187	Gln	Asp	Lys	Trp	Asp	Arg	Phe	Val	Lys	Arg	Ile	Phe	Tyr	Phe	Asn	Phe	
188		425				430					435						
190	ctg	gtc	tac	tgc	ctg	tac	atg	atc	atc	ttc	acc	atg	gct	gcc	tac	tac	2477
191	Leu	Val	Tyr	Cys	Leu	Tyr	Met	Ile	Ile	Phe	Thr	Met	Ala	Ala	Tyr	Tyr	
192	440					445				450					455		
194	agg	ccc	gtg	gat	ggc	ttg	cct	ccc	ttt	aag	atg	gaa	aaa	att	gga	gac	2525
195	Arg	Pro	Val	Asp	Gly	Leu	Pro	Pro	Phe	Lys	Met	Glu	Lys	Ile	Gly	Asp	
196				460					465					470			
198	tat	ttc	cga	ggt	act	gga	gag	atc	ctg	tct	gtg	tta	gga	gga	gtc	tac	2573
199	Tyr	Phe	Arg	Val	Thr	Gly	Glu	Ile	Leu	Ser	Val	Leu	Gly	Gly	Val	Tyr	
200			475					480					485				
202	ttc	ttt	ttc	cga	ggg	att	cag	tat	ttc	ctg	cag	agg	cgg	ccg	tcg	atg	2621
203	Phe	Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe	Leu	Gln	Arg	Arg	Pro	Ser	Met	
204			490				495					500					
206	aag	acc	ctg	ttt	gtg	gac	agc	tac	agt	gag	atg	ctt	ttc	ttt	ctg	cag	2669
207	Lys	Thr	Leu	Phe	Val	Asp	Ser	Tyr	Ser	Glu	Met	Leu	Phe	Phe	Leu	Gln	
208		505				510					515						
210	tca	ctg	ttc	atg	ctg	gcc	acc	gtg	gtg	ctg	tac	ttc	agc	cac	ctc	aag	2717
211	Ser	Leu	Phe	Met	Leu	Ala	Thr	Val	Val	Leu	Tyr	Phe	Ser	His	Leu	Lys	

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212	520				525				530				535				
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215	Glu	Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	Ala	Leu	Gly	Trp	Thr	Asn	
216					540					545				550			
218	atg	ctc	tac	tac	acc	cgc	ggt	ttc	cag	cag	atg	ggc	atc	tat	gcc	gtc	2813
219	Met	Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	Met	Gly	Ile	Tyr	Ala	Val	
220				555					560					565			
222	atg	ata	gag	aag	atg	atc	ctg	aga	gac	ctg	tgc	cgt	ttc	atg	ttt	gtc	2861
223	Met	Ile	Glu	Lys	Met	Ile	Leu	Arg	Asp	Leu	Cys	Arg	Phe	Met	Phe	Val	
224			570					575					580				
226	tac	atc	gtc	ttc	ttg	ttc	ggg	ttt	tcc	aca	gcg	gtg	gtg	acg	ctg	att	2909
227	Tyr	Ile	Val	Phe	Leu	Phe	Gly	Phe	Ser	Thr	Ala	Val	Val	Thr	Leu	Ile	
228		585					590				595						
230	gaa	gac	ggg	aag	aat	gac	tcc	ctg	ccg	tct	gag	tcc	acg	tcg	cac	agg	2957
231	Glu	Asp	Gly	Lys	Asn	Asp	Ser	Leu	Pro	Ser	Glu	Ser	Thr	Ser	His	Arg	
232	600				605					610					615		
234	tgg	cgg	ggg	cct	gcc	tgc	agg	ccc	ccc	gat	agc	tcc	tac	aac	agc	ctg	3005
235	Trp	Arg	Gly	Pro	Ala	Cys	Arg	Pro	Pro	Asp	Ser	Ser	Tyr	Asn	Ser	Leu	
236				620					625					630			
238	tac	tcc	acc	tgc	ctg	gag	ctg	ttc	aag	ttc	acc	atc	ggc	atg	ggc	gac	3053
239	Tyr	Ser	Thr	Cys	Leu	Glu	Leu	Phe	Lys	Phe	Thr	Ile	Gly	Met	Gly	Asp	
240			635					640					645				
242	ctg	gag	ttc	act	gag	aac	tat	gac	ttc	aag	gct	gtc	ttc	atc	atc	ctg	3101
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246	ctg	ctg	gcc	tat	gta	att	ctc	acc	tac	atc	ctc	ctg	ctc	aac	atg	ctc	3149
247	Leu	Leu	Ala	Tyr	Val	Ile	Leu	Thr	Tyr	Ile	Leu	Leu	Leu	Asn	Met	Leu	
248		665				670					675						
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251	Ile	Ala	Leu	Met	Gly	Glu	Thr	Val	Asn	Lys	Ile	Ala	Gln	Glu	Ser	Lys	
252	680				685				690					695			
254	aac	atc	tgg	aag	ctg	cag	aga	gcc	atc	acc	atc	ctg	gac	acg	gag	aag	3245
255	Asn	Ile	Trp	Lys	Leu	Gln	Arg	Ala	Ile	Thr	Ile	Leu	Asp	Thr	Glu	Lys	
256			700					705					710				
258	agc	ttc	ctt	aag	tgc	atg	agg	aag	gcc	ttc	cgc	tca	ggc	aag	ctg	ctg	3293
259	Ser	Phe	Leu	Lys	Cys	Met	Arg	Lys	Ala	Phe	Arg	Ser	Gly	Lys	Leu	Leu	
260		715					720				725						
262	cag	gtg	ggg	tac	aca	cct	gat	ggc	aag	gac	gac	tac	cgg	tgg	tgc	ttc	3341
263	Gln	Val	Gly	Tyr	Thr	Pro	Asp	Gly	Lys	Asp	Asp	Tyr	Arg	Trp	Cys	Phe	
264		730					735				740						
266	agg	gtg	gac	gag	gtg	aac	tgg	acc	tgg	aac	acc	aac	gtg	ggc	atc		3389
267	Arg	Val	Asp	Glu	Val	Asn	Trp	Thr	Thr	Trp	Asn	Thr	Asn	Val	Gly	Ile	
268		745				750					755						
270	atc	aac	gaa	gac	ccg	ggc	aac	tgt	gag	ggc	gtc	aag	cgc	acc	ctg	agc	3437
271	Ile	Asn	Glu	Asp	Pro	Gly	Asn	Cys	Glu	Gly	Val	Lys	Arg	Thr	Leu	Ser	
272	760				765				770					775			
274	ttc	tcc	ctg	cgg	tca	agc	aga	gtt	tca	ggc	aga	cac	tgg	aag	aac	ttt	3485
275	Phe	Ser	Leu	Arg	Ser	Ser	Arg	Val	Ser	Gly	Arg	His	Trp	Lys	Asn	Phe	
276			780					785					790				

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278 gcc ctg gtc ccc ctt tta aga gag gca agt gct cga gat agg cag tct 3533
279 Ala Leu Val Pro Leu Leu Arg Glu Ala Ser Ala Arg Asp Arg Gln Ser
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282 gct cag ccc gag gaa gtt tat ctg cga cag ttt tca ggg tct ctg aag 3581
283 Ala Gln Pro Glu Glu Val Tyr Leu Arg Gln Phe Ser Gly Ser Leu Lys
284      810      815      820
286 cca gag gac gct gag gtc ttc aag agt cct gcc gct tcc ggg gag aag 3629
287 Pro Glu Asp Ala Glu Val Phe Lys Ser Pro Ala Ala Ser Gly Glu Lys
288      825      830      835
290 tgaggacgtc acgcagacag cactgtcaac actgggcctt aggagacccc gttgccacgg 3689
292 ggggctgctg aggggaacacc agtgcctctgt cagcagcctg gcctggctctg tgctgcccc 3749
294 gcatgttccc aaatctgtgc tggacaagct gtgggaagcg ttcttgggaag catggggagt 3809
296 gatgtacatc caaccgtcac tgtccccaag tgaatctcct aacagacttt caggttttta 3869
298 ctcactttac taaaaaaaaa aaaaaaaggg cggccgctta 3909
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303 <212> TYPE: PRT
304 <213> ORGANISM: Homo sapiens
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310 Gln Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg
311 20 25 30
313 Pro Pro Pro Ala Lys Pro Gln Leu Pro Thr Ala Lys Ser Arg Thr Arg
314 35 40 45
316 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
317 50 55 60
319 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
320 65 70 75 80
322 Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
323 85 90 95
325 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
326 100 105 110
328 Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln
329 115 120 125
331 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
332 130 135 140
334 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
335 145 150 155 160
337 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
338 165 170 175
340 Leu Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn
341 180 185 190
343 Ala Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile
344 195 200 205
346 Ala Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn
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349 Gly Ala Asp Val Gln Ala Ala Ala His Gly Asp Phe Phe Lys Lys Thr
350 225 230 235 240

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